SEQUENCE LISTING

<110> Jegla, Timothy James
; ICAgen, Inc.

<120> Human HAC3

<130> 018512-002210US

<140> US 09/548,933

<141> 2000-04-13

<150> US 60/129,456

<151> 1999-04-15

<160> 16

<170> PatentIn Ver. 2.1

<210> 1

<211> 774

<212> PRT

<213> Homo sapiens

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Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His

Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val 50 55 60

Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser 65 70 75 80

Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp 85 90 95

Asp Leu Ile Met Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro 100 105 110

Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val 115 120 125

Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn 130 135 140 -

Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala 145 150 155 160

Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp 165 170 175

- Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu 185 190
- Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg 195 200 205
- Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu 210 220
- Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met 225 230 235 240
- Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly 245 250 255
- Met Met Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val 260 265 270
- Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His 275 280 285
- Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys 290 295 300
- Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val 305 310 315 320
- Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala 325 330 335
- Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser 340 345 350
- Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu 355 360 365
- Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile 370 380
- His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu 385 390 395 400
- Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn 405 410 415
- Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala 420 425 430
- Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val 435 440 445
- Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
 450 455 460
- Met Tyr Pie Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala 465 470 475 480
- Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu 485 490 495

Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys 505 510

Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu 515 520 525

Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu 530 540

Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu 545 550 555 560

Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln 565.

His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr 580 585 590

Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His 595 600 605

Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu 610 620

Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr 625 630 635 640

Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro 645 650 655

Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro 660 665 670

Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg 675 680 685

Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Arg Arg 690 695 700

Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro 705 710 715 720

Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser 725 730 735

Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
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Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
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Gln Leu Ser Ala Asn Met 770

<210> 2

<211> 2325

<212> DNA

<213> Homo sapiens

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tecetteggg tgtteggeag ceacaaagea gtggaaateg ageaggageg ggtgaagtea 240
gegggggeet ggateateca eccetacage gaetteeggt tttactggga eetgateatg 300
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cgggacacac gcctcaccga tggatcctac tttggggaga tctgcctgct aactaggggc 1500
eggegeacag ceagtgtteg ggetgacace tactgeegee tttacteact cagegtggae 1560
catttcaatg ctgtgcttga ggagttcccc atgatgcgcc gggcctttga gactgtggcc 1620
atggategge tgeteegeat eggeaagaag aatteeatae tgeageggaa gegeteegag 1680
ccaagtccag gcagcagtgg tggcatcatg gagcagcact tggtgcaaca tgacagagac 1740
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gccattgccc tgactcatca gcggggccct ctgcccctct cccctgactc tccagccacc 1920
ctecttgete getetgettg gegeteagea ggetetecag etteceeget ggtgeeegte 1980
cgagctggcc catgggcatc cacctcccgc ctgcccgccc cacctgcccg aaccctgcac 2040
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 cagegggcaa caggegatgg etetectggg egtaagggat caggaagtga geggetgeet 2220
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 <213> Artificial Sequence
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 <223> Description of Artificial Sequence: amplification
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 <400> 3
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<213> Artificial Sequence

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<210> 4
<211> 28
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:amplification
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<210> 5
<211> 24
<212> DNA
<213> Artificial Sequence
<223> Description of Artificial Sequence:amplification
      primer
<400> 5
                                                                    24
agtaggatcc atcggtgagg cgtg
<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:amplification
      primer
<400> 6
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<210> 7
<211> 29
<212> DNA
<213> Artificial Sequence
<220>
 <223> Description of Artificial Sequence:degenerate
       amplification primer
<220>
 <221> modified base
 <222> (24)
 <223> n = g, a, c or t
 <400> 7
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 <210> 8
 <211> 27
 <212> DNA
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₹220>
<223> Description of Artificial Sequence:degenerate
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<223> n = g, a, c or t
<220>
<221> modified base
<222> (25)
<223> n = g, a, c or t
<400> 8
                                                                    27
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<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:first round 5'
      RACE gene specific primer
<400> 9
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<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence
<220>
 <223> Description of Artificial Sequence:second round
       nested 5' RACL gene specific primer
 <400> 10
                                                                     25
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 <210> 11
 <211> 27
 <212> DNA
 <213> Artificial Sequence
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 <400> 11
                                                                     27
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 <210> 12
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<213> Artificial Sequence

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<210> 13
<211> 25
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:nested 3' RACE
      gene specific primer
<400> 13
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<210> 14
<211> 37
<212> DNA
<213> Artificial Sequence
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<210> 15
<211> 875
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<213> Homo sapiens
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 Thr Pro Ala Pro Gly Pro Pro Pro Pro Pro Pro Ala Pro Pro Pro Gly
 Pro Gly Pro Ala Pro Pro Gln His Pro Pro Arg Ala Glu Ala Leu Pro
          35
 Pro Glu Ala Ala Asp Glu Gly Gly Pro Arg Gly Arg Leu Arg Ser Arg
 Asp Ser Ser Cys Gly Arg Pro Gly Thr Pro Gly Ala Ala Ser Thr Ala
  65
                      70
 Lys Gly Ser Pro Asn Gly Glu Cys Gly Arg Gly Glu Pro Gln Cys Ser
                  85
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- Pro Ala Gly Pro Glu Gly Pro Ala Arg Gly Pro Lys Val Ser Phe Ser 100 105 110
- Cys Arg Gly Ala Ala Ser Gly Pro Ala Pro Gly Pro Gly Pro Ala Glu 115 120 125
- Glu Ala Gly Ser Glu Glu Ala Gly Pro Ala Gly Glu Pro Arg Gly Ser 130 135 140
- Gln Ala Ser Phe Met Gln Arg Gln Phe Gly Ala Leu Leu Gln Pro Gly 145 150 155
- Val Asn Lys Phe Ser Leu Arg Met Phe Gly Ser Gln Lys Ala Val Glu 165. 170 175
- Arg Glu Gln Glu Arg Val Lys Ser Ala Gly Ala Trp Ile Ile His Pro 180 185 190
- Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Phe Thr Met Leu Leu Phe Met 195 200 205
- Val Gly Asn Leu Ile Ile Ile Pro Val Gly Ile Thr Phe Phe Lys Asp 210 215 220
- Glu Thr Thr Ala Pro Trp Ile Val Phe Asn Val Val Ser Asp Thr Phe 225 230 235 240
- Phe Leu Met Asp Leu Val Leu Asn Phe Arg Thr Gly Ile Val Ile Glu 245 250 250
- Asp Asn Thr Glu Ile Ile Leu Asp Pro Glu Lys Ile Lys Lys Lys Tyr 260 265 270
- Leu Arg Thr Trp Phe Val Val Asp Phe Val Ser Ser Ile Pro Val Asp 275 280 285
- Tyr Ile Phe Leu Ile Val Glu Lys Gly Ile Asp Ser Glu Val Tyr Lys 290 295 300
- Thr Ala Arg Ala Leu Arg Ile Val Arg Phe Thr Lys Ile Leu Ser Leu 305 310 315
- Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp 325 330 335
- Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Met Arg 340 345 350
- Ile Cys Asn Leu Ile Ser Met Met Leu Leu Cys His Trp Asp Phe 355 360 365
- Cys Leu Gln Phe Leu Val Pro Met Leu Gln Asp Phe Pro Arg Asn Cys 370 375 380
- Trp Val Ser Ile Asn Gly Met Val Asn His Ser Trp Ser Glu Leu Tyr 385 390 395 400
- Ser Phe Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr 405 410 415

Gly Arg Gln Ala Pro Glu Ser Met Thr Asp Ile Trp Leu Thr Met Leu 420 425 430

Şer Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Ile Gly His Ala 435 440 445

Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu
450 455 460

Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala 465 470 475 480

Asp Phe Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly 485. 490 495

Lys Met Phe Asp Glu Asp Ser Ile Leu Gly Glu Leu Asn Gly Pro Leu 500 505 510

Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Ser Met 515 520 525

Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Thr 530 540

Lys Leu Lys Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu 545 550 555 560

Gly Thr Ile Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Val Ser 565 570 575

Val Leu Thr Lys Gly Asn Lys Glu Met Lys Leu Ser Asp Gly Ser Tyr 580 585 590

Phe Gly Glu Ile Cys Leu Leu Thr Arg Gly Arg Arg Thr Ala Ser Val 595 600 605

Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe 610 615 620

Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr 625 630 635 640

Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu 645 650 655

Leu His Lys Val Gln His Asp Leu Asn Ser Gly Val Phe Asn Asn Gln 660 665 670

Glu Asn Ala Ile Ile Gln Glu Ile Val Lys Tyr Asp Arg Glu Met Val 675 680 685

Gln Gln Ala Glu Leu Gly Gln Arg Val Gly Leu Phe Pro Pro Pro 690 695 700

Pro Pro Pro Gln Val Thr Ser Ala Ile Ala Thr Leu Gln Gln Ala Ala 705 710 715

Ala Met Ser Phe Cys Pro Gln Val Ala Arg Pro Leu Val Gly Pro Leu
725 730 735

Ala Leu Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala
740 745 750

Pro Ala Ala Ser Pro Gly Pro Pro Pro Pro Ala Ser Pro Pro Gly 755 760 765

Ala Pro Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu 770 775 780

Pro Ala Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser 785 790 795 800

Arg Ala Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly 805. 810 815

Ala Pro Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro 820 825 830

Arg Leu Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp 835 840 845

Arg Arg Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln 850 855 860

Asp Ser Ala Arg Ser Arg Leu Ser Ser Asn Leu 865 870 875

<210> 16

<211> 749

<212> PRT

<213> Homo sapiens

<220>

<223> human hyperpolarization-activated voltage-gated cation channel 2 (HAC2) missing amino terminus

<400> 16

Lys Glu Gln Glu Arg Val Lys Thr Ala Gly Phe Trp Ile Ile His Pro

Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Ile Met Leu Ile Met Met 20 25 30

Val Gly Asn Leu Val Ile Ile Pro Val Gly Ile Thr Phe Phe Thr Glu 35 40 45

Gln Thr Thr Thr Pro Trp Ile Ile Phe Asn Val Ala Ser Asp Thr Val

Phe Leu Leu Asp Leu Ile Met Asn Phe Arg Thr Gly Thr Val Asn Glu 65 70 75 80

Asp Ser Ser Glu Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr 85 90 95

Leu Lys Ser Trp Phe Val Val Asp Phe Ile Ser Ser Ile Pro Val Asp

Tyr Ile Phe Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr Lys 115 120 125

435

Thr Ala Arq Ala Leu Arq Ile Val Arg Phe Thr Lys Ile Leu Ser Leu 135 Leu Arg Leu Leu Arg Leu Ser Arg Leu Ile Arg Tyr Ile His Gln Trp 150 155 Glu Glu Ile Phe His Met Thr Tyr Asp Leu Ala Ser Ala Val Val Arg 170 Ile Phe Asn Leu Ile Gly Met Met Leu Leu Cys His Trp Asp Phe 185 Cys Leu Gln Phe Leu Val Pro Leu Leu Gln Asp Phe Pro Pro Asp Cys 200 Trp Val Ser Leu Asn Glu Met Val Asn Asp Ser Trp Gly Lys Gln Tyr 210 215 220 Ser Tyr Ala Leu Phe Lys Ala Met Ser His Met Leu Cys Ile Gly Tyr 235 Gly Ala Gln Ala Pro Val Ser Met Ser Asp Leu Trp Ile Thr Met Leu 250 245 Ser Met Ile Val Gly Ala Thr Cys Tyr Ala Met Phe Val Gly His Ala Thr Ala Leu Ile Gln Ser Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Met Arg Gln Lys Ile His Asp Tyr Tyr Glu His Arg Tyr Gln Gly 315 Lys Ile Phe Asp Glu Glu Asn Ile Leu Asn Glu Leu Asn Asp Pro Leu 330 325 Arg Glu Glu Ile Val Asn Phe Asn Cys Arg Lys Leu Val Ala Thr Met Pro Leu Phe Ala Asn Ala Asp Pro Asn Phe Val Thr Ala Met Leu Ser 360 Lys Leu Arg Phe Glu Val Phe Gln Pro Gly Asp Tyr Ile Ile Arg Glu 375 Gly Ala Val Gly Lys Lys Met Tyr Phe Ile Glx His Gly Val Ala Gly 390 395 Val Ile Thr Lys Ser Ser Lys Glu Met Lys Leu Thr Asp Gly Ser Tyr 405 410 Phe Gly Glu Ile Cys Leu Leu Thr Lys Gly Arg Arg Thr Ala Ser Val 425 Arg Ala Asp Thr Tyr Cys Arg Leu Tyr Ser Leu Ser Val Asp Asn Phe Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr 450 455 460

Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu 465 470 475 480

Leu Gln Lys Phe Gln Lys Asp Leu Asn Thr Gly Val Phe Asn Asn Gln 485 490 495

Glu Asn Glu Ile Leu Lys Gln Ile Val Lys His Asp Arg Glu Met Val
500 505 510

Gln Ala Ile Ala Pro Ile Asn Tyr Pro Gln Met Thr Thr Leu Asn Ser 515 520 525

Thr Ser Ser Thr Thr Thr Pro Thr Ser Arg Met Arg Thr Gln Ser Pro 530 540

Pro Val Tyr Thr Ala Thr Ser Leu Ser His Ser Asn Leu His Ser Pro 545 550 555 560

Ser Pro Ser Thr Gln Thr Pro Gln Pro Ser Ala Ile Leu Ser Pro Cys 565 570 575

Ser Tyr Thr Thr Ala Val Cys Ser Pro Pro Val Gln Ser Pro Leu Ala 580 585 590

Ala Arg Thr Phe His Tyr Ala Ser Pro Thr Ala Ser Gln Leu Ser Leu 595 600 605

Met Gln Gln Gln Pro Gln Gln Gln Gln Gln Gln Ser Gln Pro Pro Gln 610 620

Arg Gln Pro Gln Gln Pro Ser Pro Gln Pro Gln Thr Pro Gly Ser Ser 625 630 635 640

Thr Pro Lys Asn Glu Val His Lys Ser Thr Gln Ala Leu His Asn Thr 645 650 655

Asn Leu Thr Arg Glu Val Arg Pro Phe Ser Ala Trp Gln Pro Ser Leu 660 665 670

Pro His Glu Val Ser Thr Leu Ile Ser Arg Pro His Pro Thr Val Gly 675 680 685

Glu Ser Leu Ala Ser Ile Pro Gln Pro Val Thr Ala Val Pro Gly Thr 690 695 700

Gly Leu Gln Ala Gly Gly Arg Ser Thr Val Pro Gln Arg Val Thr Phe 705 710 715 720

Phe Arg Gln Met Ser Ser Gly Ala Ile Pro Pro Asn Arg Gly Val Leu
725 730 735

Pro Ala Pro Leu Pro Leu Ilo Thr Pro His Pro Lys Lys 740 745